

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a an invertebrate host, produces an RNA having:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two fully complementary RNA regions which are unrelated to do not share sequence identity with any endogenous RNA in the host, and which are in proximity to the target mRNA (a),

wherein the expressed RNA expressed by the host reduces the expression of the target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

2. (currently amended) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a an invertebrate host, produces an RNA having:

- (a) homology to at least one target mRNA expressed by the host,
- (b) an RNA region unrelated to which does not share sequence identity with any endogenous RNA in the host and is located 5' to (a) the target mRNA, and
- (c) the reverse complement of the RNA region which does not share sequence identity with any endogenous RNA in the host in (b) wherein the reverse complement is located 3' to (a) the target mRNA,

further wherein the expressed RNA expressed by the host reduces the expression of the target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

3. (withdrawn) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a host, produces an RNA having:

- (a) homology to at least one target mRNA expressed by the host, and

(b) two complementary RNA regions which are unrelated to any endogenous RNA in the host, and which are located 5' to (a), wherein the expressed RNA reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

4. (withdrawn) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a host, produces an RNA having:

(a) homology to at least one target mRNA expressed by the host, and
(b) two complementary RNA regions which are unrelated to any endogenous RNA in the host, and which are located 3' to (a), wherein the expressed RNA reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

5. (withdrawn) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a host, produces an RNA having:

(a) homology to at least one target mRNA expressed by the host, and
(b) two complementary RNA regions which are unrelated to any endogenous RNA in the host, and which are located within (a), wherein the expressed RNA reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

6. (currently amended) The recombinant construct of any of Claims 1-5 1-2 wherein the RNA region or regions which are unrelated to do not share sequence identity with any endogenous RNA in the host comprise a synthetic, non-naturally occurring RNA sequence.

7. (currently amended) The recombinant construct of any of Claims 1-5 1-2 wherein the RNA region or regions which are unrelated to do not share sequence identity with any endogenous RNA in the host do not comprise plant viral RNA.

8. (currently amended) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by an invertebrate host based on the Clustal method of alignment, which comprises the method comprising:

- (a) transforming a host with any of the recombinant constructs of Claims 4-5 1-2; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA that has at least

80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

9. (currently amended) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment, which comprises the method comprising:

- (a) transforming a host with the recombinant construct of Claim 6; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

10. (currently amended) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by an invertebrate host based on the Clustal method of alignment, which comprises the method comprising:

- (a) transforming a host with the recombinant construct of Claim 7; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

11. (currently amended) An RNA comprising:

- (a) homology to at least one target mRNA expressed by a an invertebrate host, and
- (b) two fully complementary RNA regions which are unrelated to do not share sequence identity with any endogenous RNA in the host, and which are in proximity to (a) the target mRNA, wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

12. (currently amended) An RNA comprising:

- (a) homology to at least one target mRNA expressed by a an invertebrate host,

- (b) an RNA region unrelated to which does not share sequence identity with any endogenous RNA in the host and is located 5' to (a) the target mRNA, and
- (c) the reverse complement of the RNA region which does not share sequence identity with any endogenous RNA in the host in (b) located 3' to (a) the target mRNA, wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

Claim 13. (withdrawn) An RNA comprising:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are unrelated to any endogenous RNA in the host, and which are located 5' to (a), wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 14. (withdrawn) An RNA comprising:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are unrelated to any endogenous RNA in the host, and which are located 3' to (a), wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 15. (withdrawn) An RNA comprising:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are unrelated to any endogenous RNA in the host, and which are located within (a), wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

16. (currently amended) The RNA of any of Claims 41-15 11-12 wherein the RNA region or regions which are unrelated to do not share sequence identity with any endogenous RNA in the invertebrate host comprise a synthetic, non-naturally occurring RNA sequence.

17. (currently amended) The RNA of any of Claims 41-15 11-12 wherein the RNA region or regions which are unrelated to do not share sequence identity with any endogenous RNA in the invertebrate host do not comprise plant viral RNA.

18. (currently amended) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment, which comprises the method comprising:

- (a) introducing into a host any of the RNA of Claims 41-15 11-12; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

19. (currently amended) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by an invertebrate host based on the Clustal method of alignment, which comprises the method comprising:

- (a) introducing into a host the recombinant construct of Claim 16; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA that has at least 80% sequence identity with the RNA expressed by the host based on the Clustal method of alignment.

Claim 20. (withdrawn) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA which comprises:

- (a) introducing into a host the recombinant construct of Claim 17; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 21. (withdrawn) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a host produces an RNA having:

- (a) homology to at least one target mRNA expressed by the host,
- (b) two complementary RNA regions which are encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is

substantially similar to the target mRNA and said regions are in proximity to (a),

wherein the expressed RNA reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 22. (withdrawn) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a host, produces an RNA having:

- (a) homology to at least one target mRNA expressed by the host,
- (b) an RNA region encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA and located 5' to (a), and
- (c) the reverse complement of the nucleic acid in (b) located 3' to (a),

wherein the expressed RNA reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

23. (withdrawn) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a host, produces an RNA having:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA, and which regions are located 5' to (a),

wherein the expressed RNA reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 24. (withdrawn) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a host, produces an RNA having:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA, and which regions are located 3' to (a),

wherein the expressed RNA reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 25. (withdrawn) A recombinant construct comprising a promoter operably linked to a DNA sequence which, when expressed by a host, produces an RNA having:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA, and which regions are located within (a),

wherein the expressed RNA reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 26. (withdrawn) The recombinant constructs of Claims 21-25 wherein the nucleic acid sequence in the genome of the host is a sequence which is not expressed by the host.

Claim 27. (withdrawn) The recombinant constructs of Claims 21-25 wherein the nucleic acid sequence in the genome of the host is sequence which is expressed by the host.

Claim 28. (withdrawn) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA which comprises:

- (a) transforming a host with any of the recombinant constructs of Claims 21-25; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 29. (withdrawn) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA which comprises:

- (a) transforming a host with the recombinant construct of Claim 26; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 30. (withdrawn) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA which comprises:

- (a) transforming a host with the recombinant construct of Claim 27; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 31. (withdrawn) An RNA comprising:

- (a) homology to at least one target mRNA expressed by a host,
- (b) two complementary RNA regions which are encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA and which regions are in proximity to (a),

wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 32. (withdrawn) An RNA comprising:

- (a) homology to at least one target mRNA expressed by a host,
- (b) an RNA region encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA and is located 5' to (a), and
- (c) the reverse complement of the RNA in (b) located 3' to (a),

wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 33. (withdrawn) An RNA comprising:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA and which regions are located 5' to (a),

wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 34. (withdrawn) An RNA comprising:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA, and which regions are located 3' to (a),

wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 35. (withdrawn) An RNA comprising:

- (a) homology to at least one target mRNA expressed by the host, and
- (b) two complementary RNA regions which are encoded by any nucleic acid sequence in the genome of the host provided that said sequence does not encode the target mRNA or any sequence that is substantially similar to the target mRNA, and which are located within (a),

wherein the RNA, when introduced into the host, reduces the expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 36. (withdrawn) The RNA of any of Claims 31-35 wherein the nucleic acid sequence in the genome of the host is a sequence which is not expressed by the host.

Claim 37. (withdrawn) The RNA of any of Claims 31-35 wherein the nucleic acid sequence in the genome of the host is a sequence which is expressed by the host.

Claim 38. (withdrawn) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA which comprises:

- (a) introducing into a host any of the RNA of Claims 31-35; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 39. (withdrawn) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA which comprises:

- (a) introducing into a host the RNA of Claim 36; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 40. (withdrawn) A method for reducing expression of a target mRNA or any substantially similar endogenous mRNA which comprises:

- (a) introducing into a host the RNA of Claim 37; and
- (b) selecting hosts which have reduced expression of the target mRNA or any substantially similar endogenous mRNA.

Claim 41. (withdrawn) A method for identifying or screening an essential plant gene which comprises:

- (a) transforming a plant cell with a recombinant construct comprising a constitutive promoter wherein said construct is capable of reducing expression of an essential plant gene with a high degree of frequency;
- (b) quantifying all transformed plant cells from step (a);
- (c) quantifying all transformed plant cells from a control which does not reduce expression of an essential plant gene; and
- (d) comparing the quantification of transformed plant cells selected from step (b) with the quantification of transformed plants cells selected from step (c) wherein the quantification of transformed plants cells selected from step (c) should substantially exceed the quantification of transformed plant cells selected from step (b).

Claim 42. (withdrawn) A method for identifying or screening an essential plant gene which comprises:

- (a) transforming a plant cell with the recombinant construct of any of Claims 1-5 which further comprises a constitutive promoter which is capable of reducing expression of an essential plant gene with a high degree of frequency;
- (b) quantifying all transformed plant cells from step (a);
- (c) quantifying all transformed plant cells from a control which does not reduce expression of an essential plant gene; and
- (d) comparing the quantification of transformed plant cells selected from step (b) with the quantification of transformed plants cells selected from step (c) wherein the quantification of transformed plants cells selected from step (c) should substantially exceed the quantification of transformed plant cells selected from step (b).

Claim 43. (withdrawn) A method for identifying or screening an essential plant gene which comprises:

- (a) transforming a plant cell with the recombinant construct of any of Claim 6 which further comprises a constitutive promoter which is capable of reducing expression of an essential plant gene with a high degree of frequency;
- (b) quantifying all transformed plant cells from step (a);

- (c) quantifying all transformed plant cells from a control which does not reduce expression of an essential plant gene; and
- (d) comparing the quantification of transformed plant cells selected from step (b) with the quantification of transformed plants cells selected from step (c) wherein the quantification of transformed plants cells selected from step (c) should substantially exceed the quantification of transformed plant cells selected from step (b).

Claim 44. (withdrawn) A method for identifying or screening an essential plant gene which comprises:

- (a) transforming a plant cell with the recombinant construct of any of Claim 7 which further comprises a constitutive promoter which is capable of reducing expression of an essential plant gene with a high degree of frequency;
- (b) quantifying all transformed plant cells from step (a);
- (c) quantifying all transformed plant cells from a control which does not reduce expression of an essential plant gene; and
- (d) comparing the quantification of transformed plant cells selected from step (b) with the quantification of transformed plants cells selected from step (c) wherein the quantification of transformed plants cells selected from step (c) should substantially exceed the quantification of transformed plant cells selected from step (b).

45. (currently amended) The recombinant construct of Claims 4-5 1-2 wherein the DNA sequences encoding the two fully complementary RNA sequences regions are comprised within any of the sequences set forth in SEQ ID NOs: 12, 13, or 34.